

SUPPORT FOR THE AMENDMENTS

The Title of the application has been amended as suggested by the Examiner.

The stringent conditions now specified in Claim 1 are supported by the specification at page 14, line 22 to page 15, line 15. The other amendments to this claim remove the phrase "in Sequence Listing."

Newly added Claims 27-44 are supported by Claims 2-10.

No new matter is believed to have been added to this application by these amendments.

REMARKS

Claims 1-44 are pending. Favorable reconsideration is respectfully requested.

The rejection of Claims 1-3, 7, and 11 under 35 U.S.C. §101 is believed to be obviated by the amendment submitted above. As amended, Claim 1 is clearly directed to a non-natural microorganism. Accordingly, withdrawal of this rejection is respectfully requested.

The rejection of the claims under 35 U.S.C. §112, second paragraph, is believed to be obviated by the amendments submitted above in part and is, in part, respectfully traversed.

The term "inversion" has been removed from the claims.

With respect to the term "increased" in the amended claims, one skilled in the art reading the claims in light of the present specification would readily appreciate that the expression amount is increased relative to that of the unmodified bacterium.

Claims 2, 3, 7, and 11 are not indefinite simply because they embrace non-elected subject matter. Since Claim 1 is generic, Applicants respectfully request that examination continue on that claim.

Based on the foregoing, withdrawal of this ground of rejection is respectfully requested.

Applicants submit that the rejection of the claims under 35 U.S.C. §112, first paragraph, as set forth in paragraph (9) of the Official Action dated December 7, 2001 is believed to be obviated by the amendments submitted above. Claim 1 has been amended to recite stringent conditions in (B), (D), (F), and (H). Accordingly, withdrawal of this ground of rejection is respectfully requested.

The rejection of the claims under 35 U.S.C. §112, first paragraph, as set forth in paragraph (10) of the Official Action dated December 7, 2001 is believed to be obviated by the amendments submitted above.

Claim 1 has been amended to recite stringent conditions in (B), (D), (F), and (H).

In addition, once a sequence has been described, one skilled in the art would recognize various methods for increasing the copy number thereof. Also, once a target protein has been described, one skilled in the art would recognize various methods for increasing the expression amount of the protein.

Moreover, it is well-known that glutamic acid, lysine, and proline are an acidic amino acid, a basic amino acid, and an imino acid, respectively, are differ widely in their properties. Even so, similar improvements are obtained as shown in the present specification. Therefore, the improvement in the productivity of the other amino acids is believed to be reasonably expected.

Based on the foregoing, the claims are enabled. Withdrawal of this ground of rejection is respectfully requested.

The rejection of amended Claims 1, 2, 11, and 12 under 35 U.S.C. §102(e) over U.S. patent No. 6,040,160 (U.S. ‘160) is respectfully traversed.

Claim 1 has been amended to recite stringent conditions in (B), (D), (F), and (H). As such, Applicants submit that U.S. '160 fails to described the claimed bacterium. Accordingly, withdrawal of this ground of rejection is respectfully requested.

The rejection of amended Claims 1, 2, and 11-13 under 35 U.S.C. §103(a) over Blattner et al. in view of Vrijic et al. and U.S. '160 is respectfully traversed.

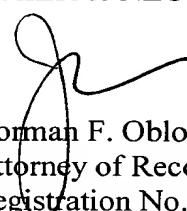
Based on "DR" (Pfam; PF018101 LysE; 1) of Blatter et al., the Examiner appears to take the position that the YAHN polypeptide, based on sequence homology using the Pfam database, belongs to the LysE family.

However, as seen from the Pfam accession number PF01810, a copy of which is attached to the Information Disclosure Statement (IDS) submitted herewith, the fact that the YAHN polypeptide belongs to the LysE protein family is based on the publication Trends Biochem. Sci. 1999; 24:133-125 (a copy of the PubMed search result is attached for that publication; see the IDS submitted herewith), which was published in April 1999, i.e., after the priority date of the present application. Therefore, the rejection is believed to be unsustainable, and withdrawal of the same is respectfully requested.

Applicants submit that the present application is in condition for allowance. Early notice to this effect is earnestly solicited.

Respectfully submitted,

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Serial No.: 09/459,573
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IN THE TITLE

Please amend the title as follows.

Page 1, first line, please replace the Title with the following:

--ESCHERICHIA BACTERIA OVEREXPRESSING THE YAHN GENE FOR
FEEDBACK-INSENSITIVE AMINO ACID PRODUCTION--.

IN THE CLAIMS

Please amend the claims as follows.

--1. (Amended) A bacterium belonging to the genus *Escherichia* and having an ability to produce an L-amino acid, which has been modified to increase [wherein the ability to produce the L-amino acid is increased by increasing] an expression amount of at least one protein selected from the group consisting of the following proteins of (A) to (H):

(A) a protein having an amino acid sequence shown in SEQ ID NO: 10 [in Sequence Listing];

(B) a protein which is encoded by a DNA which hybridizes with the nucleotide sequence shown in SEQ ID NO: 9 under stringent conditions of 60°C, 1x SSC and 0.1% SDS [has an amino acid sequence including deletion, substitution, insertion, addition or inversion of one or several amino acids in the amino acid sequence shown in SEQ ID NO: 10 in Sequence Listing], and which has an activity of increasing the ability to produce the L-amino acid of the bacterium having the protein;

(C) a protein having an amino acid sequence shown in SEQ ID NO: 12 [in Sequence Listing];

(D) a protein which is encoded by a DNA which hybridizes with the nucleotide sequence shown in SEQ ID NO: 11 under stringent conditions of 60°C, 1x SSC and 0.1% SDS [has an amino acid sequence including deletion, substitution, insertion, addition or inversion of one or several amino acids in the amino acid sequence shown in SEQ ID NO: 12 in Sequence Listing], and which has an activity of increasing the ability to produce the L-amino acid of the bacterium having the protein;

(E) a protein having an amino acid sequence shown in SEQ ID NO: 14 [in Sequence Listing];

(F) a protein which is encoded by a DNA which hybridizes with the nucleotide sequence shown in SEQ ID NO: 13 under stringent conditions of 60°C, 1x SSC and 0.1% SDS [has an amino acid sequence including deletion, substitution, insertion, addition or inversion of one or several amino acids in the amino acid sequence shown in SEQ ID NO: 14 in Sequence Listing], and which has an activity of increasing the ability to produce the L-amino acid of the bacterium having the protein;

(G) a protein having an amino acid sequence shown in SEQ ID NO: 16 [in Sequence Listing]; or

(H) a protein which is encoded by a DNA which hybridizes with the nucleotide sequence shown in SEQ ID NO: 15 under stringent conditions of 60°C, 1x SSC and 0.1% SDS [has an amino acid sequence including deletion, substitution, insertion, addition or inversion of one or several amino acids in the amino acid sequence shown in SEQ ID NO: 16 in Sequence Listing], and which has an activity of increasing the ability to produce the L-amino acid of the bacterium having the protein.--

Claims 27-44 (New).